

EXHIBIT 12

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVKLSLIDUIGNSFYESTULTRALSSQFMLSISEASDNLKRSDDMFSGLNVPFYGWQ  
LWTWGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTH  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFY  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPOAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSVKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
msqnksafmqpvnsadlaaivgagmppteiiikmwdyikenslqdpnkrninpddkl  
akvfgtekpdmfamtkmvsqhiik
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *SEQ ID 2*

Sequence 2 lcl|seq_2 Length 86 *PROBST SEQ ID NO 5*

N significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site. Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use Mega BLAST Strand option

Open gap and extension gap penalties

Gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

Sequence in FASTA format from: to:

```
SIIVALSLLDDTGNSFYESTDTHALSSQFMLSISEASONQKRSDDMDFSGLNVFRIGWQG  
NTWGWAKTQDPEPASSATITDPQKANRFHRTLTLTLWLPAGYVPSPKHRSPLIANTLWGNM  
LATESLKNSAELTFSDFPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQHT  
SLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
GENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAFFLGALGIYSSLSHFTVEVGAYPRS  
STKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
SPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRP
```

Sequence 2 Enter accession or GI or download from file

Sequence in FASTA format from: to:

```
vgagpmprteiikkmwdyikenslqdpnkrninpddklakvfgtekipdmfemtkmvsq
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

LAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965

Sequence 2 lcl|seq_2 Length 61

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#).

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVKLSLIDUIGNSPYESTDLTRALSSQPLSLISEASUNQLRSDDMFSGLNVPYIGWQG  
LWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHCHHFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
aatscelanqhghlqfp1l1trsl1ml1psqsqshr
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 **SEQ ID NO: 2**

Sequence 2 lcl|seq_2 Length 36 **Probst SEQ ID NO: 7**

N significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSUVKLSLIDIGNSFYESTDLTHALSSQFMLSISEASUNQLKSDDMDFSGLNVPHYGWQJ  
LWTWGWAKTQDPEPASSATITDPQKANRFHRTLTLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTTLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINLVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
lrhhaslqtnmdisnfpf
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lc|seq_1 Length 965 *seq id no: 2*

Sequence 2 lc|seq_2 Length 18 *Probst seq id no: 8*

N significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVLSLIDUIGNSFYESTDLTRALSSQPLSLSEASUNQLRSDDMLFSGLNVPHYGWLG  
LWTGWAKTDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQHTT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVLAYQPVLVYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

lalwn

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: gap extension:

x_dropoff: expect: wordsize: Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *SEQ ID NO. 2*

Sequence 2 lcl|seq_2 Length 5 *Probst seq in no. 9*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☒ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSUVKLSLLDDYGNSTPSTDLTHALSSQFMLSISEASDNQLKSDUMDFSGLNVPFIQWQ  
LWTWGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCFFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ccyrvnhhid
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: gap extension:

x_dropoff: expect: wordsize: Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *SEQ ID NO: 2*

Sequence 2 lcl|seq_2 Length 11 *Probst SEQ ID NO: 10*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use **MegaBLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSUVKLSLIDUIGNSFYESTDLTHALSSQFMLSISEASUNQLKSDDMDFSGLNVPHYGWQG  
LWTWGWAKTQDEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSELTTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHY  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCCHFYT  
QGENLTSQGTFRSQTMGGAFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVLAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYSKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
vdvividsvaalvpkselegeigdvhvgqlqarmmsq
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: gap extension: x_dropoff: expect: wordsize: Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965

SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 36

Probst SEQ ID NO: 11

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use Mega BLAST Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVKLSLIDYGNSTYESTDLTHALSSQFMLSISEASDNQLRSDDMDFSGLNVPHTGWQJ  
LWTWGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHY  
FSLKFSQTYTKLNERYAKNNVSSKNYSQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
mpriigidipakkkkisltyigipalskeiiaarlqlnpearaaglteeevgrlnallqs  
dyvvegdlrrrvqsdkrlitihayrgqrhrslpvrqqrktksrtrkgkrktiagkkk
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lc|seq_1 Length 965

SEQ ID NO: 2

Sequence 2 lc|seq_2 Length 121

Probst SEQ ID NO: 12

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☐ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file
r sequence in FASTA format from: to:

```
LSDVRLSLDDYGNSTESTDLTHALSSQFALSI SEASUNQLKSDUMDFSGLNVPHYGWQG  
LWTWGWARTQDPEPASSATITDPQKANRFHRTLTLTLWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLPSLQEGFLLTKLVGLYSYGDHNCHEFT  
QGENLTSQGTFRSQTMGGAVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLPVIGVGSFMNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file
or sequence in FASTA format from: to:

```
rptnkrninpddklakvfgt
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**

x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965 *seq id no: 2*

Sequence 2 lcl|seq_2 Length 20 *probst seq id no: 13*

No significant similarity was found

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using **BLAST** engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in **BLASTN** program only:

Reward for a match: Penalty for a mismatch:

☒ Use **Mega BLAST** Strand option

Open gap and extension gap penalties

gap x_dropoff expect word size Filter ☒

Sequence 1 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
LSDVRLSLDDIGNSFYESTDLTHALSSQFMLSISEASDNQLKSDUDMFSGLNVPHTGWQG  
LWTGWAKTQDPEPASSATITDPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNM  
LLATESLKNSAELTPSDHPPFWGITGGGLGMMVYQDPRENHPGFHMRSSGYSAGMIAGQTHT  
FSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCHEFYT  
QGENLTSQGTFRSQTMGGAFFDLPMKPFGSTHILTAFFLGALGIYSSLSHFTEVGAYPRS  
FSTKTPLINVLVPIGVKGSFMMNATQRPQAWTVLAYQPVLYRQEPGIATQLLASKGIWFGS  
GSPSSRHAMSYKISQQTQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
```

Sequence 2 Enter accession or GI or download from file

or sequence in FASTA format from: to:

```
ddklakvfgtekipdmfgmt
```

Comments and suggestions to blast-help@ncbi.nlm.nih.gov



Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☒ **Align**

Sequence 1 lcl|seq_1 Length 965

SEQ ID NO: 2

Sequence 2 lcl|seq_2 Length 20

Probst SEQ ID NO: 14

No significant similarity was found